
FRED 2 – An Immunoinformatics Framework for Python

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Method	Version	Usage	Platform Compatibility	Reference
MHC binding:				
SYFPEITHI	1.0	T-cell epitope	Windows, Linux, Mac	(Rammensee, et al., 1999)
BIMAS	1.0	MHC-I binding	Windows, Linux, Mac	(Parker, et al., 1994)
SVMHC	1.0	MHC-I binding	Windows, Linux, Mac	(Dönnes and Elofsson, 2002)
ARB	1.0	MHC-I binding	Windows, Linux, Mac	(Bui, et al., 2005)
SMM	1.0	MHC-I binding	Windows, Linux, Mac	(Peters and Sette, 2005)
SMMPMBEC	1.0	MHC-I binding	Windows, Linux, Mac	(Kim, et al., 2009)
Epidemix	1.1	MHC-I binding	Windows, Linux, Mac	(Feldhahn, et al., 2009)
Complib Sidney 2008	1.0	MHC-I binding	Windows, Linux, Mac	(Sidney, et al., 2008)
PickPocket*	1.1	MHC-I binding	Linux, Mac	(Zhang, et al., 2009)
NetMHC*	3.0, 3.4	MHC-I binding	Linux, Mac	(Lundegaard, et al., 2008)
NetMHCpan*	2.4, 2.8	MHC-I binding	Linux, Mac	(Hoof, et al., 2009)
HAMMER	1.0	MHC-II binding	Windows, Linux, Mac	(Sturniolo, et al., 1999)
TEPIPOPEpan	1.0	MHC-II binding	Windows, Linux, Mac	(Zhang, et al., 2012)
NetMHCII*	2.2	MHC-II binding	Linux, Mac	(Nielsen, et al., 2007)
NetMHCIIpan*	3.0, 3.1	MHC-II binding	Linux, Mac	(Karosiene, et al., 2013)
UniTope	1.0	T-cell epitope	Windows, Linux, Mac	(Toussaint, et al., 2011)
NetCTLpan*	1.1	T-cell epitope	Linux, Mac	(Stranzl, et al., 2010)
Cleavage Prediction:				
ProteaSMM (C/S20)	1.0	Cleavage site	Windows, Linux, Mac	(Tenzer, et al., 2005)
PCM	1.0	Cleavage site	Windows, Linux, Mac	(Dönnes and Kohlbacher, 2005)
NetChop*	3.1	Cleavage site	Linux, Mac	(Nielsen, et al., 2005)
Ginodi	1.0	Cleavage fragment	Windows, Linux, Mac	(Ginodi, et al., 2008)
TAP Prediction:				
SVMTAP	1.0	TAP affinity	Windows, Linux, Mac	(Dönnes and Kohlbacher, 2005)
SMMTAP	1.0	TAP affinity	Windows, Linux, Mac	(Peters, et al., 2003)
Additive matrix method	1.0	TAP affinity	Windows, Linux, Mac	(Doytchinova, et al., 2004)
Epitope Selection:				
OptiTape ⁺	1.0	Epitope selection for vaccine design	Windows, Linux, Mac	(Toussaint and Kohlbacher, 2009)
Epitope Assembly:				
TSP approach ⁺	1.0	String-of-beads design	Windows, Linux, Mac	(Toussaint, et al., 2011)
Spacer design + TSP ⁺	1.0	Spacer design	Windows, Linux, Mac	(Schubert and Kohlbacher, 2016)
HLA Typing:				
OptiType*	1.0	MHC-I typing	Linux, Mac	(Szolek, et al., 2014)

Polysolver*	1.0	MHC-I typing	Linux, Mac	(Shukla, et al., 2015)
Seq2HLA*	2.2	MHC-I/II typing	Linux, Mac	(Boegel, et al., 2013)
ATHLATES*	1.0	MHC-I/II typing	Linux, Mac	(Liu, et al., 2013)

* Installation of external software is required.

+ An integer linear programming solver such as CBC (<https://projects.coin-or.org/Cbc>) is required. For Epitope assembly the LKH approximation software (<http://www.akira.ruc.dk/~keld/research/LKH/>) is advised to use.

The integrated tools were chosen due to their wide spread use and high accuracy (Backert and Kohlbacher, 2015). Some methods mentioned by Backert et al. could not be integrated due to lack of publicly available stand-alone software or inadequate description of the method. However, FRED 2 was designed to be easily extendable by providing well defined interfaces as well as tutorials dedicated to developers (<https://github.com/FRED-2/Fred2/wiki>). We explicitly encourage users to contribute to FRED 2 and extend its capabilities by integrating new prediction methods or by extending its capabilities.

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